

Run on: July 31, 2002, 15:19:17 ; Search time 30.12 Seconds

(without alignments)  
62.691 Million cell updates/sec

Title: US-09-641-802-2  
Perfect score: 89  
Sequence: 1 LQTPQLQVMMEPGD 17

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

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Maximum Match 100%
Listing first 45 summaries
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Database :

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21:	/SIDS1/gcgdata/hold-geneseq/genseqp-emb1/AA2000.DAT.*
22:	/SIDS1/gcgdata/hold-geneseq/genseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	89	100.0	17	22	AAE072247	Colostrinin derivative
2	89	100.0	17	22	AAE072501	Colostrinin peptid
3	89	100.0	17	22	AAE072533	Colostrinin peptid
4	89	100.0	17	22	AAE059310	Ewe colostrinin pe
5	89	100.0	18	22	AAE059341	Ewe colostrinin pe
6	56	62.9	11	22	AAE07195	Colostrinin peptid
7	56	62.9	12	22	AAE07195	Modified colostrin
8	46	51.7	12	22	AAE07195	S. pneumoniae elon
9	46	51.7	693	19	AAE08722	Streptococcus pneu
10	46	51.7	693	22	AAU37640	CFE 96 protein seq
11	45	50.6	83	22	AAE01093	peptide #2023 enco
					ABE29372	

[illegible]

PT Infections, comprises administering colostrinin as an immunological  
 PT regulator -  
 XX  
 PS Claim 1; Page 34; 50pp; English.  
 XX  
 CC Sequences AAB72246 - AAB72275 represent peptides derived from colostrinin,  
 CC a proline rich polypeptide aggregate contained in colostrum. The  
 CC peptides have immune response modulatory activity, and are capable of  
 CC inducing cytokines. Colostrinin and its derived peptides are useful for  
 CC inducing cytokine production, for modulating an immunological response  
 CC and for inducing blood cell proliferation. The peptides are useful in the  
 CC treatment of disorders of the central nervous system, neurological  
 CC disorders, mental disorders, dementia, neurodegenerative diseases,  
 CC Alzheimer's disease, motor neurone disease, psychosis, neurosis, chronic  
 CC disorders of the immune system, bacterial and viral infections and  
 CC acquired immunological deficiencies.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLQVMEPGD 17  
 DB 1 lqtpqpllyqymepgd 17

RESULT 2  
 AAB72501  
 ID AAB72501 standard; Peptide; 17 AA.  
 XX  
 AC AAB72501;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #2.  
 XX  
 KM Dermatological; oxidative stress regulator; colostrinin.  
 XX  
 OS unidentified.  
 XX  
 PN WO200112650-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000MO-US22665.  
 XX  
 PR 17-AUG-1999; 99US-0149310.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Stanion GJ, Hughes TK, Boldogh I;  
 XX  
 DR WPI: 2001-218342/22.  
 XX  
 PT Modulating oxidative stress level in a cell, involves contacting the  
 PT cell with an oxidative stress regulator selected from colostrinin, its  
 PT constituent peptide, analog or their combinations -  
 XX  
 PS Claim 6; Page 25; 48pp; English.  
 XX  
 CC The present invention relates to a method for modulating the oxidative  
 CC stress level in a cell or a patient, comprising contacting the cell with,  
 CC or administering to the patient, an oxidative stress regulator selected  
 CC from colostrinin, or its constituent peptide (e.g. the present peptide),  
 CC to change the level of an oxidizing species in the cell. The method can  
 CC be used to treat oxidative damage to skin, by decreasing or preventing an  
 CC increase in the level of damage to a biomolecule of the patient.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLQVMEPGD 17  
 DB 1 lqtpqpllyqymepgd 17

RESULT 3  
 AAB72533  
 ID AAB72533 standard; Peptide; 17 AA.  
 XX  
 AC AAB72533;  
 XX  
 DT 09-MAY-2001 (first entry)  
 XX  
 DE Colostrinin peptide #2.  
 XX  
 KM Neuroprotective; neural cell differentiation regulator; colostrinin;  
 KM colostrum.  
 XX  
 OS unidentified.  
 XX  
 PN WO200112651-A2.  
 XX  
 PD 22-FEB-2001.  
 XX  
 PF 17-AUG-2000; 2000MO-US22774.  
 XX  
 PR 17-AUG-1999; 99US-0149633.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Boldogh I;  
 XX  
 DR WPI: 2001-226545/23.  
 XX  
 PT Use of colostrinin, its constituent peptide or analog as a neural cell  
 PT regulator, for promoting neural cell differentiation and treating  
 PT damaged neural cells in a patient -  
 XX  
 PS Claim 6; Page 21; 35pp; English.  
 XX  
 CC The present invention relates to a method for promoting neural cell  
 CC differentiation and treating damaged neural cells, using colostrinin and  
 CC colostrinin constituent peptides (e.g. the present peptide) as a neural  
 CC cell regulator. Colostrinin is a polypeptide complex found in colostrum.  
 XX  
 SQ Sequence 17 AA;

Query Match 100.0%; Score 89; DB 22; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-07;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 LQTPQPLQVMEPGD 17  
 DB 1 lqtpqpllyqymepgd 17

RESULT 4  
 AAB59310  
 ID AAB59310 standard; Peptide; 17 AA.  
 XX  
 AC AAB59310;  
 XX  
 DT 21-MAR-2001 (first entry)  
 XX  
 DE Ewe colostrinin peptide fragment A-1.  
 XX  
 KM Sheep; colostrinin; proline rich polypeptide; colostrum; immune disorder;

DR WPI; 2001-071058/08.  
XX  
PT Bertidos having an X

PT Peptides having an N-terminal amino acid sequence isolated from PT colostrin for treating e.g. disorders of the central nervous system and immune system, viral and bacterial infections, and diseases characterized by amyloid plaques -

PS Claim 8; Page 27; 63pp; English.

CC The present invention provides the sequences of a number of peptides

central nervous system disorders such as senile dementia, Parkinson's

disorders such as bacterial and viral infections, to improve the

development of a child's immune system, as a dietary supplement, and to promote the dissolution of beta-amyloid plaques.

PT characterized by amyloid plaques  
XX  
PS Claim 7; Page 27; 63pp; English..  
XX

Query Match	100.0%	Score 89; DB 23;	Length 18;
Best Local Similarity	100.0%	Pred. No. 13e-07;	
Matches 17; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

ОУ 1 ЛОТРОПІОВМЕРОД 17

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QY      1 LQTPQPLQYVMEPEQGD 17
          | | | | | | | | | |
Db      2 lqtqppllqymnepeqgd 18

RESULT  6
ID      AAE07185
        AAE07185 standard: neotrid

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AAE07185
ID   AAE07185 standard; peptide; 11 aa.
XX
AC   AAE07185:
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Matches	17;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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DT	06-NOV-2001	(first entry)
XX		
DE	colostrin1n	peptide 1.
XX		

Db 1 lqtpqpl1qvmnēpgd 17

KM	Colostrinum; nootropic; neuroprotective; immunomodulatory; antibacterial;
KM	Parkinson's disease; Alzheimer's disease; mental disorder; food additive;
KM	central nervous system disorder; neurodegenerative disorder; weight loss;
KM	beta-amyloid plaque; psychosis; neurosis; cachexia; motor neuron disease;

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1D AAB59341 standard; 18 AA.  
XX

PN W0200155100-27

AC AAB59341;  
XX

03-ATTG-2001  
 PN

21-MAR-2001 (first entry)

Ewe colostrinin peptide fragment derived sequence #1.

26-JAN-2000. 2000CB-0001825

central nervous system disorder; dietary supplement; beta-amyloid plaque;

05 0v1s sp.

FR  
Georg J. J.

PN WO200075173-A2.

[illegible]

PD 14-DEC-2000.  
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02-JUN-2000; 2000WO-GB02128.

PR 02-JUN-1999; 99GB-0012852.

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(REGE-) REGEN THERAPEUTICS PLC.

## Mathematical models

Georgiades JA;  
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VY

Example 2; Page 8; 40pp; English.

genes



derived from mRNA of human breast, and then measuring the label

cc nuclear level: the present sequence is a peptide encoded by a single exon  
cc nucleic acid probe of the invention.

CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 83 AA;

Query Match 50.6%; Score 45; DB 22; Length 83;  
 Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 OY 1 LGTPPPLQVMEPQ 15  
 || ||||| : ||  
 21 lqkppllasiaspq 35

Standard; Protein; 83 AA.

19955;

DT 23-JAN-2002 (first entry)

DE Protein #1954 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;  
 KW cardiovascular disease; hypertension; cardiac arrhythmia;  
 KW congenital heart disease.

OS Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

PT Single exon nucleic acid probes for analyzing gene expression in human

PT hearts -

PS Claim 15; SEQ ID NO 21725; 530pp; English.

CC The present invention relates to single exon nucleic acid probes for  
 CC measuring human gene expression in a sample derived from human heart (see  
 CC ABA21535-ABA41305). The present sequence is a protein encoded by one such  
 CC probe. The probes may be used for predicting, measuring and displaying  
 CC gene expression in samples derived from the human heart via microarrays.  
 CC By measuring gene expression, the probes are useful for predicting,  
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the  
 CC human heart and vascular system e.g. cardiovascular disease,  
 CC hypertension, cardiac arrhythmias and congenital heart disease.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

SQ Sequence 83 AA;

Query Match 50.6%; Score 45; DB 22; Length 83;

Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LGTPPPLQVMEPQ 15  
 || ||||| : ||  
 Db 21 lqkppllasiaspq 35

RESULT 14

ID AAM55332 standard; Protein; 83 AA.

AC AAM55332;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 27437.

KW Human; brain expressed exon; gene expression analysis; probe;

KW microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;  
 KW epilepsy; cancer.

OS Homo sapiens.

PN WO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human

PT brains -

PS Example 4; SEQ ID NO: 27437; 650pp + Sequence Listing; English.

CC The present invention provides a number of single exon nucleic acid  
 CC probes which are derived from genomic sequences expressed in the human  
 CC brain. They can be used to measure gene expression in brain cell samples,  
 CC which may enable the diagnosis and improved treatment of nervous system  
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,  
 CC epilepsy and cancers. The present sequence is a protein encoded by one of  
 CC the probes of the invention.

SQ Sequence 83 AA;

Query Match 50.6%; Score 45; DB 22; Length 83;  
 Best Local Similarity 60.0%; Pred. No. 7.1;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;  
 OY 1 LGTPPPLQVMEPQ 15  
 || ||||| : ||  
 Db 21 lqkppllasiaspq 35

RESULT 15

AAM67729 standard; Protein; 83 AA.

XX

AC AAM67729;

XX 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 28035.

KW Human; bone marrow expressed exon; gene expression analysis; probe;

XX microarray; cancer; leukaemia; lymphoma; myeloma.

OS Homo sapiens.

XX WO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00668.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488900/53.

Human genome-derived single exon nucleic acid probes useful for  
analyzing gene expression in human bone marrow -

Example 4; SEQ ID NO: 28035; 658bp + Sequence Listing; English.

The present invention provides a number of single exon nucleic acid  
probes which are derived from genomic sequences expressed in the human  
bone marrow. They can be used to measure gene expression in bone marrow  
samples, which may enable the improved diagnosis and treatment of cancers  
such as lymphoma, leukaemia and myeloma. The present sequence is a  
sequence encoded by one of the probes of the invention.

83 AA;

RESULT

ID ABB1995 13

AC ABB1995 13

XX ABB1995 13

50.6%; Score 45; DB 22; Length 83;

60.0%; Pred. No. 7.1;

Conservative 1; Mismatches 5; Indels 0; Gaps 0;

VMMEPQ 15

slaspg 35

Completed: July 31, 2002, 15:23:25  
Time: 248 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:21:17 ; Search time 12.85 Seconds

(without alignments)  
32.314 Million cell updates/sec

Title: US-09-641-802-2

Perfect score: 89

Sequence: 1 LQTPQPLQVMPEQD 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA:\*

1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*

2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*

3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*

4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*

5: /cgn2\_6/ptodata/2/1aa/6C.COMB.pep:\*

6: /cgn2\_6/ptodata/2/1aa/Backfillseq1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	50.6	667	2	US-08-718-661-2
2	41	46.1	343	3	US-08-858-003-32
3	41	46.1	343	3	US-09-078-166-32
4	41	46.1	343	4	US-08-997-467-32
5	41	46.1	428	4	US-09-347-833-6
6	40.5	45.5	369	2	US-08-596-291-4
7	40.5	45.5	369	3	US-09-100-804-4
8	40.5	45.5	369	5	PCT-US94-09943-4
9	40	44.9	671	3	US-09-121-321-16
10	40	44.9	671	4	US-08-933-803A-16
11	38.5	43.3	179	4	US-08-858-207A-456
12	38	42.7	1276	4	US-09-297-937C-13
13	37	41.6	328	4	US-09-225-244-2
14	37	41.6	328	4	US-09-417-242-2
15	36.5	41.0	2441	1	US-08-194-468-2
16	36.5	41.0	2441	3	US-08-961-739-2
17	36	40.4	210	1	US-08-078-090-2
18	36	40.4	213	4	US-09-131-028A-2
19	36	40.4	213	4	US-09-131-028A-12
20	36	40.4	366	3	US-08-945-056-8
21	36	40.4	390	1	US-08-335-583C-2
22	36	40.4	615	3	US-08-860-091A-4
23	36	40.4	618	3	US-08-834-306-65
24	36	40.4	618	4	US-08-993-674A-65
25	36	40.4	1106	4	US-08-180-195-2
26	36	40.4	1106	1	US-08-168-917-2
27	36	40.4	1106	1	US-08-477-329-2

28	36	40.4	1106	2	US-08-475-458-2	Sequence 2, Appl1
29	36	40.4	1106	2	US-08-460-510-2	Sequence 2, Appl1
30	36	40.4	1106	2	US-08-460-490-2	Sequence 2, Appl1
31	36	40.4	1106	3	US-08-980-400-2	Sequence 2, Appl1
32	36	40.4	1106	3	US-08-462-728-4	Sequence 4, Appl1
33	36	40.4	1106	4	US-09-583-459A-2	Sequence 2, Appl1
34	36	40.4	1106	4	US-09-583-210-2	Sequence 2, Appl1
35	36	40.4	1106	4	US-09-583-449A-2	Sequence 2, Appl1
36	36	40.4	1106	5	PCT-US92-00720-2	Sequence 2, Appl1
37	36	40.4	1106	5	PCT-US92-00862-2	Sequence 2, Appl1
38	36	40.4	4545	2	US-08-804-227C-14	Sequence 14, Appl1
39	36	40.4	4550	2	US-08-804-227C-8	Sequence 8, Appl1
40	36	40.4	4550	2	US-08-804-198-2	Sequence 2, Appl1
41	35	39.3	357	1	US-08-638-911A-37	Sequence 37, Appl1
42	35	39.3	439	3	US-08-993-359-24	Sequence 24, Appl1
43	35	39.3	439	3	US-09-221-654-2	Sequence 2, Appl1
44	35	39.3	439	3	US-08-989-358A-2	Sequence 2, Appl1
45	35	39.3	504	1	US-07-932-915-2	Sequence 2, Appl1

#### ALIGNMENTS

```

RESULT 1
US-08-718-661-2
; Sequence 2, Application US/08718661
; Patent No. 5876972
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Nucleic acid molecules coding for mammalian
; TITLE OF INVENTION: tumor suppressor proteins and methods for their isolation
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,661
; FILING DATE:
; CLASSIFICATION: 530
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 667 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-718-661-2

Query Match          50.6%; Score 45; DB 2; Length 667;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      1 LQTPQPLQVMPEQ 15
DB      543 LPVPQPLPQPMQ 557

RESULT 2
US-08-858-003-32
; Sequence 32, Application US/08858003
; Patent No. 6060234
; GENERAL INFORMATION:
; APPLICANT: Katz, Leonard
; APPLICANT: Stassl, Diane L.
; APPLICANT: Summers Jr., Richard G.
; APPLICANT: Ruan, Xiaolan
; APPLICANT: Pereda-Lopez, Ana
; APPLICANT: Kakavas, Stephan J.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES
; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME
; NUMBER OF SEQUENCES: 34

```

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Abbott Laboratories  
;; STREET: 100 Abbott Park Rd.  
;; CITY: Abbott Park  
;; STATE: Illinois  
;; COUNTRY: USA  
;; ZIP: 60064-3500  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FASTSEQ Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/858, 003  
;; FILING DATE: 16-MAY-1979  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Dianne Casuto  
;; REGISTRATION NUMBER: P-40,943  
;; REFERENCE/DOCKET NUMBER: 4952.US.P2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (847)-938-3137  
;; TELEFAX: (847)-938-2623  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 343 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: No. 6060234e  
;; US-08-858-003-32

Query Match 46.1%; Score 41; DB 3; Length 343;  
Best Local Similarity 46.7%; Pred. No. 41;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPQLQVMMEPOG 16  
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Db 42 QLPRPLKDVLEAPEG 56

RESULT 3  
US-09-078-166-32  
; Sequence 32, Application US/09078166  
; Patent No. 6063561  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Leonard  
; APPLICANT: Stassl, Diane L.  
; APPLICANT: Summers Jr., Richard G.  
; APPLICANT: Ruan, Xiaocan  
; APPLICANT: Pereda-Lopez, Ana  
; APPLICANT: Kakavas, Stephan J.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES  
; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Rd.  
; CITY: Abbott Park  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/078,166  
;; FILING DATE: 16-MAY-1979  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Dianne Casuto  
;; REGISTRATION NUMBER: P-40,943  
;; REFERENCE/DOCKET NUMBER: 4952.US.P2  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (847)-938-3137  
;; TELEFAX: (847)-938-2623  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 32:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 343 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: No. 6063561e  
;; US-09-078-166-32

Query Match 46.1%; Score 41; DB 3; Length 343;  
Best Local Similarity 46.7%; Pred. No. 41;  
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPQLQVMMEPOG 16  
| : | | : : |  
Db 42 QLPRPLKDVLEAPEG 56

RESULT 4  
US-08-997-467-32  
; Sequence 32, Application US/08997467  
; Patent No. 6200813  
; GENERAL INFORMATION:  
; APPLICANT: Katz, Leonard  
; APPLICANT: Stassl, Diane L.  
; APPLICANT: Summers Jr., Richard G.  
; APPLICANT: Ruan, Xiaocan  
; APPLICANT: Pereda-Lopez, Ana  
; APPLICANT: Kakavas, Stephan J.  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES  
; TITLE OF INVENTION: AND RECOMBINANT METHODS FOR MAKING SAME  
; NUMBER OF SEQUENCES: 34  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Abbott Laboratories  
; STREET: 100 Abbott Park Rd.  
; CITY: Abbott Park  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60064-3500  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/997,467  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/858,003  
; FILING DATE: 16-MAY-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dianne Casuto  
; REGISTRATION NUMBER: P-40,943  
; REFERENCE/DOCKET NUMBER: 4952.US.P2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (847)-938-3137  
; TELEFAX: (847)-938-2623

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TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 343 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6200813e
US-08-997-467-32

Query Match          46.1%; Score 41; DB 4; Length 343;
Best Local Similarity 46.7%; Pred. No. 41;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMEPQG 16
| : : : : : : :
DB 42 QLPRLKDVLEAFEG 56

RESULT 5
US-09-347-833-6
; Sequence 6, Application US/09347833
; Patent No. 6294658
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Layo O.
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: Factors Involved in Gene Expression
; FILE REFERENCE: BB-1172
; CURRENT APPLICATION NUMBER: US/09/347,833
; EARLIER FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Glycine max
US-09-347-833-6

Query Match          46.1%; Score 41; DB 4; Length 428;
Best Local Similarity 46.7%; Pred. No. 52;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPQPLQVMEPQG 16
| : : : : : : :
DB 273 QQPMPMQQMLPRG 287

RESULT 6
US-08-596-291-4
; Sequence 4, Application US/08596291
; Patent No. 5821075
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/596,291
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: 10461/7000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; TELEX: 92-1742 EZEKIEL
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-596-291-4

Query Match          45.5%; Score 40.5; DB 2; Length 369;
Best Local Similarity 47.4%; Pred. No. 53;
Matches 9; Conservative 5; Mismatches 2; Indels 3; Gaps 1;

QY 2 QTP---QPLQVMEPQGD 17
| : | | | | : : :
DB 268 KTPDSAQPLQMLDVEED 286

RESULT 7
US-09-100-804-4
; Sequence 4, Application US/09100804
; Patent No. 6066472
; GENERAL INFORMATION:
; APPLICANT: GONEZ, LEONEL JORGE
; APPLICANT: SARAS, JAN
; APPLICANT: CLAESSON-WELSH, LENA
; APPLICANT: HELDIN, CARL-HENRIK
; TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
; TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,804
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/596,291
; FILING DATE: 09-AUG-1996
; APPLICATION NUMBER: US 08/115,573
; FILING DATE: 01-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/09943
; FILING DATE: 01-SEP-1994
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Query Match	45.5%	Score 40.5;	DB 5;	Length 369;
Best Local Similarity	47.4%	Pred. No. 53;		
Matches	9;	Conservative	5;	Mismatches 2;
				Indels 3;
				Gaps 1.
Qy	2	OTP---	OPLOVMEPOGD	17
Db	268	KTFPSAQFLQALMDV	EEED	286

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RESULT          9
US-09-121-321-16
: Sequence 16, Application US/09121321
: Patent No. 6090783
: GENERAL INFORMATION:
:   APPLICANT: Saiga, Akihiko
:   APPLICANT: Orita, Satoshi
:   APPLICANT: Igarashi, Hisanaga
:   APPLICANT: Okumura, Kouichi
:   APPLICANT: Sakaguchi, Gaku
: TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF
:   TITLE OF INVENTION: GENE EXPRESSION AND NOVEL PROTEIN
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: FISH & NEAVE
:   STREET: 1251 Avenue of the Americas
:   CITY: New York
:   STATE: New York
:   COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC/compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
:   APPLICATION NUMBER: US/09/121,321
:   FILING DATE:
:   CLASSIFICATION:
:   PRIOR APPLICATION DATA:
:     APPLICATION NUMBER: US 08/933,803
:     FILING DATE: 19-SEP-1997
:     ATTORNEY/AGENT INFORMATION:
:       NAME: Haley, James F.
:       REGISTRATION NUMBER: 27,794
:       REFERENCE/DOCKET NUMBER: SHGN-12CIP
:     TELECOMMUNICATION INFORMATION:
:       TELEPHONE: 212-596-9000
:       TELEFAX: 212-596-9090
:     INFORMATION FOR SEQ ID NO: 16:
:       SEQUENCE CHARACTERISTICS:
:         LENGTH: 671 amino acids
:         TYPE: amino acid
:         TOPOLOGY: linear
:       MOLECULE TYPE: protein
: US-09-121-321-16

Query Match          44.9%: Score 40; DB 3; Length 671;
Best Local Similarity 57.1%: Pred. No. 1.2e+02;
Matches      8; Conservative      1; Mismatches      5; Indels      0; Gaps      0.

QY      2 QTPQPLQVMEPQ 15
          1 11111111
Db      415 QPQQLQSQPQPQ 428

RESULT      10
US-09-933-803A-16
: Sequence 16, Application US/08933803A
: Patent No. 6218522
: GENERAL INFORMATION:
:   APPLICANT: Saiga, Akihiko
:   APPLICANT: Orita, Satoshi

```

APPLICANT: Igarashi, Hisanaga  
APPLICANT: Okumura, Kouichi  
TITLE OF INVENTION: DNA MOLECULE RELATING TO SUPPRESSION OF  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/933,803A  
FILING DATE: 19-SEP-1997  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Haley, James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHCN-12CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-596-9000  
TELEFAX: 212-596-9090  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 671 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-933-803A-16

Query Match 44.9%; Score 40; DB 4; Length 671;  
Best Local Similarity 57.1%; Pred. No. 1.2e+02;  
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QTPPQLQVMEPQ 15  
DB 415 QPPQPOLQSQPQPQ 428

RESULT 11  
US-08-858-207A-456  
; Sequence 456, Application US/08858207A  
; Patent No. 6348328  
; GENERAL INFORMATION:  
; APPLICANT: Black, Michael  
; APPLICANT: Hodgson, John  
; APPLICANT: Knowles, David  
; APPLICANT: Nicholas, Richard  
; APPLICANT: Stodola, Robert  
; TITLE OF INVENTION: No. 6348328e1 Compounds  
; NUMBER OF SEQUENCES: 552  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Smithkline Beecham Corporation  
; STREET: 709 Swedeland Road  
; CITY: King of Prussia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19406-0939  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/858,207A

FILING DATE: 09-MAY-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/017670  
FILING DATE: 14-MAY-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmil, Edward R.  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50475  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 456:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 179 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6348328e  
US-08-858-207A-456

Query Match 43.3%; Score 38.5; DB 4; Length 179;  
Best Local Similarity 47.1%; Pred. No. 49;  
Matches 8; Conservative 4; Mismatches 2; Indels 3; Gaps 1;

QY 4 PQLPQV--MMEPQD 17  
DB 88 PQLPQVTSFGLPQD 104

RESULT 12  
US-09-297-937C-13  
; Sequence 13, Application US/09297937C  
; Patent No. 6337199  
; GENERAL INFORMATION:  
; APPLICANT: YUM, DO Young  
; APPLICANT: PAN, Jae Gu  
; TITLE OF INVENTION: Membrane-Bound Glucanase Dehydrogenase, Gene Sequence  
; TITLE OF INVENTION: Encoding the Same and Production of 2-Keto-D-Gluconate  
; FILE REFERENCE: P66159USO  
; CURRENT APPLICATION NUMBER: US/09/297,937C  
; CURRENT FILING DATE: 1999-05-11  
; PRIOR APPLICATION NUMBER: PCT/KR98/00296  
; PRIOR FILING DATE: 1998-09-25  
; PRIOR APPLICATION NUMBER: KR 97-48802  
; PRIOR FILING DATE: 1997-09-25  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1276  
; TYPE: PRT  
; ORGANISM: Erwinia cyrillipedi  
US-09-297-937C-13

Query Match 42.7%; Score 38; DB 4; Length 1276;  
Best Local Similarity 53.8%; Pred. No. 5.2e+02;  
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQTPPQLQVME 13  
DB 826 LKNPGLVQAMMK 838

RESULT 13  
US-09-225-244-2  
; Sequence 2, Application US/09225244  
; Patent No. 6018038  
; GENERAL INFORMATION:  
; APPLICANT: Boung-Jun OH

```

; APPLICANT: Moon Kyung KO
; APPLICANT: Igor KOSTENYUK
; TITLE OF INVENTION: Incompatible Plant and Pathogen Interaction Related Gene
; FILE REFERENCE: 1942/35
; CURRENT APPLICATION NUMBER: US/09/225,244
; CURRENT FILING DATE: 1999-01-04
; EARLIER APPLICATION NUMBER: No. 6018038 Yet Assigned
; EARLIER FILING DATE: Concurrent Herewith
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Wordperfect 6.1 Windows
; SEQ ID NO 2
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Capsicum annuum
; US-09-225-244-2

Query Match      41.6%; Score 37; DB 3; Length 328;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 LGTPQPLQVMEPQG 16
      ::||| | | |
Db      27 VRKEPPLQANSDPNG 42

RESULT 14
US-09-417-242-2
; Sequence 2, Application US/09417242
; Patent No. 6252049
; GENERAL INFORMATION:
; APPLICANT: Bounng-Jun OH
; APPLICANT: Moon Kyung KO
; APPLICANT: Igor KOSTENYUK
; TITLE OF INVENTION: Incompatible Plant and Pathogen Interaction Related Gene
; FILE REFERENCE: 1942/35
; CURRENT APPLICATION NUMBER: US/09/417,242
; CURRENT FILING DATE: 1999-10-12
; EARLIER APPLICATION NUMBER: US 09/225,244
; EARLIER FILING DATE: 1999-01-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Wordperfect 6.1 Windows
; SEQ ID NO 2
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Capsicum annuum
; US-09-417-242-2

Query Match      41.6%; Score 37; DB 4; Length 328;
Best Local Similarity 37.5%; Pred. No. 1.7e+02;
Matches 6; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 LGTPQPLQVMEPQG 16
      ::||| | | |
Db      27 VRKEPPLQANSDPNG 42

RESULT 15
US-08-194-468-2
; Sequence 2, Application US/08194468
; Patent No. 5750336
; GENERAL INFORMATION:
; APPLICANT: Montminy, Marc R.
; TITLE OF INVENTION: ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF CAMP AND MITOGEN
; TITLE OF INVENTION: RESPONSIVE GENES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretly, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California

```

```

; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/194,468
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)-546-4737
; TELEFAX: (619)-546-9392
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-194-468-2

Query Match      41.0%; Score 36.5; DB 1; Length 2441;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 10; Conservative 0; Mismatches 5; Indels 5; Gaps 1;

QY      2 QTPQPLQ---VMEPQG 16
      ||||| | | | |
Db      1902 QTPQPPAQPPSPVNMSPAG 1921

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Search completed: July 31, 2002, 15:23:44  
Job time: 147 sec







GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:21:52 ; Search time 15.13 Seconds

(without alignments)  
107.966 Million cell updates/sec

Title: US-09-641-802-2

Perfect score: 89

Sequence: 1 LGTPQPLQVMEPEQD 17

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	53.9	709	2	D86907 elongation factor
2	47.5	53.4	192	2	AF1753 Orf150 (bacteriophage
3	46	51.7	639	2	S03268 tetracycline resis
4	46	51.7	693	2	B95032 translation elonga
5	46	51.7	693	2	B97903 elongation factor
6	44	49.4	134	2	S44430 synuclein - human
7	44	49.4	134	2	S39046 phosphonoprotein
8	44	49.4	137	2	I56498 phosphonoprotein
9	44	49.4	671	2	C96534 conserved Poly-A Bl
10	43	48.3	134	2	AB0784 tetracycline resis
11	43	48.3	639	2	S13142 tetracycline resis
12	43	48.3	639	2	A60633 tetracycline resis
13	43	48.3	639	2	A56779 tetracycline resis
14	43	48.3	695	2	AE1406 translation elonga
15	43	48.3	695	2	AE1782 translation elonga
16	43	48.3	699	2	E97594 translation elonga
17	43	48.3	699	2	AC2816 translation elonga
18	43	48.3	844	2	F86231 hypotehtical prote
19	42	47.2	263	2	S74353 carbonic anhydrase
20	42	47.2	580	2	S13328 hypotehtical prote
21	42	47.2	595	2	F85438 nucleoporin-like p
22	42	47.2	643	2	S55610 polypeptide - equi
23	42	47.2	698	2	C82332 translation elonga
24	41	46.1	78	2	D91160 hypotehtical prote
25	41	46.1	78	2	E65136 hypotehtical 8.7 k
26	41	46.1	78	2	C86006 hypotehtical prote
27	41	46.1	639	2	A24333 tetracycline resis
28	41	46.1	641	2	JN0800 tetracycline-mnuc
29	41	46.1	857	2	JC4169 phosphoenolpyruv

30	41	46.1	1058	1	WMBE52 UL52 protein - hum
31	41	46.1	1653	2	B91052 hypotehtical prote
32	41	46.1	1653	2	G65028 hypotehtical prote
33	41	46.1	1653	2	F85896 hypotehtical prote
34	40.5	45.5	549	2	S53427 protein-tyrosine-p
35	40.5	45.5	656	1	A55574 protein-tyrosine-p
36	40.5	45.5	656	1	JC4263 protein-tyrosine-p
37	40	44.9	237	2	G72676 hypotehtical prote
38	40	44.9	259	2	T14439 hypotehtical prote
39	40	44.9	282	2	T14440 hypotehtical prote
40	40	44.9	284	2	T47277 lactoylgutathione
41	40	44.9	300	2	T21149 hypotehtical prote
42	40	44.9	357	2	E96696 protein F1N21.10 l
43	40	44.9	357	2	T38405 hypotehtical prote
44	40	44.9	380	2	H87344 esterase, probable
45	40	44.9	691	1	EFTWG translation elonga

## ALIGNMENTS

RESULT 1  
D86907 elongation factor G [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
C:Species: Lactococcus lactis subsp. lactis  
C:Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
C:Accession: D86907  
R:Bolotin, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarne, K.; Weissenbach, J.; Ehr  
Genome Res. 11, 731-753, 2001  
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis  
A:Reference number: A86625; MUID:21235186; PMID:11337471  
A:Accession: D86907  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-709 <STO>  
A:Cross-references: GB:AE005176; PID:g12725331; PID:AAK06358.1; GSPDB:GN00146  
A:Experimental source: strain IL1403  
C:Genetics:  
A:Gene: fusa  
C:superfamily: translation elongation factor G; translation elongation factor Tu homo

Query Match 53.9%; Score 48; DB 2; Length 709;  
Best Local Similarity 40.0%; Pred. No. 5.6;  
Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

QY 1 LGTPQPLQVMEPEQ 15  
DB 415 IEVPEVQLMVEPK 429

RESULT 2  
AF1753 [bacteriophage b11285] homolog 1ln2571 [imported] - Listeria innocua (strain C1  
C:Species: Listeria innocua  
C:Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AF1753  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec  
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurgey, O.; Entian, K.D.; Fshih,  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;  
Ok, C.; Schluter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla  
A:Title: Comparative genomes of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AF1753  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-192 <GLA>  
A:Cross-references: GB:AL592022; PID:CA97798.1; PID:g16415093; GSPDB:GN00178  
A:Experimental source: strain C1p11262  
C:Genetics:  
A:Gene: 1ln2571



A:Title: A new brain-specific 14-kDa protein is a phosphoprotein. Its complete amino acid sequence is deduced from complementary DNA  
A:Reference number: S39046; MUID:94039126  
A:Accession: S39046  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-134 <NAK>  
R:Nakajo, S.; Tsunada, K.; Omata, K.; Nakamura, Y.; Nakaya, K.  
Submitted to JIPID, October 1993  
A:Description: A new brain-specific 14-kDa protein is a phosphoprotein: Its complete amino acid sequence is deduced from complementary DNA  
A:Reference number: JU0238  
A:Accession: JU0238  
A:Molecule type: protein  
A:Residues: 1-134 <NA2>  
!Keywords: brain

Query Match	49.4%	Score 44	DB 2	Length 134
Best Local Similarity	46.2%	Pred. No. 4		
Matches	6	Mismatches	1	Gaps 0
		Conservative		

```
QY      5 QPLQVMMERQGD 17
          :|:::|::|:
Db     105 EPLIEPMEPEGE 117
```

RESULT 8  
I56498  
phosphonuroprotein 14 - rat  
C:Species: Rattus sp. (rat)  
C:Date: 26-Jul-1996 #sequence-revision 26-Jul-1996 #text-change 05-Nov-1999  
C:Accession: I56498  
R:Tobe, T.; Nakajo, S.; Tanaka, A.; Miya, A.; Omata, K.; Nakaya, K.; Tomita, M.; Nakam  
J. Neurochem. 59, 1624-1629, 1992  
A:Title: Cloning and characterization of the cDNA encoding a novel brain-specific 14-kDa  
A:Reference number: I56498; M01D:93019240  
A:Accession: I56498  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-137 <RFS>  
A:Cross-references: GB:D17764; NID:g409780; PIDN:BA04610.1; PID:g459235

Query Match	49.4%	Score 44	DB 2	Length 137
Best Local Similarity	46.28%	Pred. No. 4.1		
Matches 6; Conservative		Mismatches 1	Indels 0	Gaps 0

```
QY      5 QPLQVMEPEGD 17
          :||: :|||:|:
Db     105 EPLIEPLMEPEG 117
```

RESULT 9

C96534

probable Poly A Binding Protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001

R:Theorist: C96534

R:Thesaurus: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: C96534

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-671 <STO>

A:Cross-references: GB:AE005173; NID:g10120431; PIDN:AAIG31056.1; GSFDB:GN00141

C:Genetics:  
A:Gene: F14022.3  
A:Map position: 1  
C:Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology

Query Match	49.4%	Score 44:	DB 2;	Length 671;
Best Local Similarity	46.7%	Pred. No. 25;		
Matches 7; Conservative	3;	Mismatches 5;	Indels 0;	Gaps 0;

```
QY      2 QTPQPLQVMMERQG 16
          | | | : | | | : |
Db     514 QQPSPMMQQQMHPRG 528
```

RESULT 10  
AB0784  
conserved hypothetical protein STY2446 [imported] - *Salmonella enterica* subsp. *enterica*  
C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh  
A:Note: This species has also been called *Salmonella typhi*  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AB0784  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church  
th, T.; Connerton, J.R.; Croplin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* se  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AB0784  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-134 <PAR>  
A:Cross-references: GB:AL513382; PIDN:G16503449; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY2446

Query Match	48.3%	Score 43	DB 2	Length 134
Best Local Similarity	61.5%	Pred. No. 5.9		
Matches	8	Conservative	1	Mismatches 4
				Indels 0
				Gaps 0

```
QY      2 QTPQLQVMEP 14
          | | | | | : |
Db      63 QAPQLRQSM LSP 75
```

RESULT 11  
S13142

C>Date: 13-Jan-1995 #sequence\_revision 10-Feb-1995 #text\_change 02-Feb-2001  
C/Accession: S13142  
R/Burdet, V.  
Nucleic Acids Res. 18, 6137, 1990  
A>Title: Nucleotide sequence of the tet(M) gene of Tn916.  
A/Reference number: S13142; MUID: 91045089  
A/Accession: S13142  
A/Molecule type: DNA  
A/Residues: 1-639 <BGR>  
A/Cross-references: EMBL:X56353; NID:947061; PIDN:CMA39796.1; PID:947062  
R/Burdet, V.  
J. Biol. Chem. 266, 2872-2877, 1991  
A>Title: Purification and characterization of Tet(M), a protein that renders ribosome  
A/Reference number: A23749; MUID: 91131580  
A/Contents: annotation; function; amino end of purified recombinant protein  
A/Note: protein purified after expression in E. coli shown to be ribosome-dependent  
A/Genetics:  
A/Gen: tetM  
C/Superfamily: translation elongation factor G; translation elongation factor Tu homo  
C/Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop  
F4-131/Domain: translation elongation factor Tu homology <ETU>  
F10-17/Region: nucleotide-binding motif A (P-loop)

F:128-131/Region: GTP-binding NKXD motif  
F:220-222/Region: GTP-binding SAK/L motif  
F:16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 48.3% Score 43; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 35;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQTPPLQVMEP 14  
Db 339 IENPHPLQTTVEP 352

RESULT 12  
A60633  
tetraacycline resistance protein - Staphylococcus aureus (strain MRSA101)  
C:Species: Staphylococcus aureus  
C>Date: 28-Apr-1993 #sequence\_revision 28-Apr-1993 #text\_change 02-Feb-2001  
C:Accession: A60633  
R:Neslin, M.; Svec, P.; Lupski, J.R.; Godson, G.N.; Kreiswirth, B.; Kornblum, J.; Projan, R.; Neill, M.; Agents Chemother. 34, 2273-2276, 1990  
A:Title: Cloning and nucleotide sequence of a chromosomally encoded tetracycline resistance gene  
A:Reference number: A60633; MUID:91158314  
A:Accession: A60633  
A:Molecule type: DNA  
A:Residues: 1-639 <NDS>  
A:Cross-references: GB:M21136; NID:g153114; PIDN:AAA26678.1; PID:g153115  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homolog  
C:Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop  
F:10-11/Domain: translation elongation factor Tu homology <ETU>  
F:10-11/Region: nucleotide-binding motif A (P-loop)  
F:128-131/Region: GTP-binding NKXD motif  
F:220-222/Region: GTP-binding SAK/L motif  
F:16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 48.3% Score 43; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 35;  
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQTPPLQVMEP 14  
Db 339 IENPHPLQTTVEP 352

RESULT 13  
A56779  
tetraacycline resistance protein TetM - Enterococcus faecalis transposon Tn916  
C:Species: Enterococcus faecalis  
C>Date: 08-Sep-1995 #sequence\_revision 08-Sep-1995 #text\_change 02-Feb-2001  
C:Accession: A56779  
R:Su, Y.A.; He, P.; Clewell, D.B.  
A:Antimicrob. Agents Chemother. 36, 769-778, 1992  
A:Title: Characterization of the tetM determinant of Tn916: evidence for regulation by a reference number: A56779; MUID:92368175  
A:Reference number: A56779; MUID:92368175  
A:Accession: A56779  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-639 <SDU>  
A:Cross-references: GB:M55225; NID:g148321; PIDN:AAA24784.1; PID:g148322  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homolog  
C:Keywords: antibiotic resistance; GTP binding; nucleotide binding; P-loop  
F:4-13/Domain: translation elongation factor Tu homology <ETU>  
F:10-11/Region: nucleotide-binding motif A (P-loop)  
F:128-131/Region: GTP-binding NKXD motif  
F:220-222/Region: GTP-binding SAK/L motif  
F:16,17,55,128,129,131,220/Binding site: Mg-GTP (Lys, Thr, Thr, Asn, Lys, Asp, Ser) #sta

Query Match 48.3% Score 43; DB 2; Length 639;  
Best Local Similarity 50.0%; Pred. No. 35;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQTPPLQVMEP 14  
Db 339 IENPHPLQTTVEP 352

RESULT 14  
AE1406  
translation elongation factor G homolog fus [imported] - Listeria monocytogenes (strain C-27)  
C:Species: Listeria monocytogenes  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AE1406  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maltounam, A.; Ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla, A.; Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1406  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-695 <GLA>  
A:Experimental source: strain EGD-e  
C:Genetics:  
A:Gene: fus  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homolog

Query Match 48.3% Score 43; DB 2; Length 695;  
Best Local Similarity 40.0%; Pred. No. 38;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPPLQVMEP 15  
Db 399 MEPEPVIOVAIEPK 413

RESULT 15  
AE1782  
translation elongation factor G homolog fus [imported] - Listeria innocua (strain C11)  
C:Species: Listeria innocua  
C>Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 14-Dec-2001  
C:Accession: AE1782  
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihl, D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A:Authors: Krefl, J.; Kuhn, M.; Kunst, F.; Kurapkak, G.; Madueno, E.; Maltounam, A.; Ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla, A.; Title: Comparative genomics of Listeria species.  
A:Reference number: AB1077; MUID:21537279; PMID:11679669  
A:Accession: AE1782  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-695 <GLA>  
A:Experimental source: strain C11p1262  
C:Genetics:  
A:Gene: fus  
C:Superfamily: translation elongation factor G; translation elongation factor Tu homolog

Query Match 48.3% Score 43; DB 2; Length 695;  
Best Local Similarity 40.0%; Pred. No. 38;  
Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTPPLQVMEP 15  
Db 399 MEPEPVIOVAIEPK 413

Wed Jul 31 15:17:27 2002

us-09-641-802-2.rpr

Page 5

Search completed: July 31, 2002, 15:24:07  
Job time: 135 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 31, 2002, 15:23:47 ; Search time 10.34 Seconds  
(without alignments)  
63.659 Million cell updates/sec

Title: US-09-641-802-2

Perfect score: 89  
Sequence: 1 LQRPQLQVMMEPGD 17

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	53.9	691	1 EFG_STRPY	P82477 streptococ
2	46	51.7	639	1 TETM_UREUR	P09757 ureaplasma
3	44	49.4	134	1 SYUB_BOVIN	P33567 bos taurus
4	44	49.4	134	1 SYUB_HUMAN	Q16143 homo sapien
5	44	49.4	137	1 SYUB_RAT	Q63754 rattus norv
6	43	48.3	639	1 TETM_ENTFA	P21598 enterococcu
7	43	48.3	639	1 TETM_STRAU	Q53770 staphylococ
8	43	48.3	699	1 EFG_AGRU	P70782 agrobacteri
9	42	47.2	643	1 VP40_HSEVE	P52369 equine herp
10	41	46.1	78	1 YHGG_ECOLI	P46845 escherichia
11	41	46.1	544	1 TCPEG_DROME	P48605 drosophila
12	41	46.1	639	1 TETM_ENTFA	P11131 enterococcu
13	41	46.1	639	1 TETM_STRAU	Q54807 streptococ
14	41	46.1	641	1 TETM_LISMO	Q48791 listeria mo
15	41	46.1	646	1 TETM_LACIA	Q48712 lactococcus
16	41	46.1	857	1 CAPP_THES7	P51060 thermus sp.
17	41	46.1	1058	1 UL52_HSV1	P10236 herpes simp
18	40	44.9	282	1 LGUL_BRAOL	Q39366 brasica ol
19	40	44.9	357	1 YFDB_SCHPO	Q10170 schizosacch
20	40	44.9	671	1 Z282_HUMAN	Q94477 homo sapien
21	40	44.9	691	1 EFG2_SYNY3	P74228 synchocyst
22	40	44.9	691	1 EFG_THETH	P13551 thermus aqu
23	40	44.9	1161	1 POL_SFY1	P23074 simian foam
24	39	43.8	249	1 GRPE_SYNY3	Q59978 synchocyst
25	39	43.8	341	1 EFG_STRRA	P29541 streptomyce
26	39	43.8	612	1 GAG_JSVRV	P31622 sheep pulmo
27	39	43.8	618	1 MTOI_HUMAN	Q9Y222 homo sapien
28	39	43.8	639	1 TETM_NEIME	Q51238 neisseria m
29	39	43.8	674	1 RNE_SYNY3	P72656 synchocyst
30	39	43.8	679	1 YKRS_YRST	P34227 saccharomyc
31	39	43.8	708	1 EFGI_STRCO	P40173 streptomyce
32	39	43.8	758	1 PSAA_PEA	P05310 pisum sativ
33	39	43.8	962	1 PTRR_ECOLI	P05458 escherichia

## ALIGNMENTS

RESULT	1	STANDARD	PRT	691 AA.
AC	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	16-OCT-2001 (Rel. 40, Last annotation update)			
GN	FUS OR SPY0273.			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;			
OX	Streptococcus.			
NCBI_TaxID=1314;				
NP	SEQUENCE FROM N.A.			
RC	STRAIN-SF370 / ATCC 700294 / Serotype M1;			
RX	MEDLINE-21192684; PubMed-11296296;			
RA	Ferrecci J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,			
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,			
RA	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,			
RA	Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;			
RT	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).			
RN	[2]			
RP	PARTIAL SEQUENCE, AND MASS SPECTROMETRY.			
RC	STRAIN-JRS4 / Serotype M6;			
RA	Hogan D.A., Du P., Stevenson T.I., Whilton M., Kilby G.W., Rogers J.,			
RA	Vanborgele R.A.;			
RT	"Two-dimensional gel electrophoresis map of Streptococcus pyogenes			
RL	proteins.";			
CC	Submitted (MAY-2000) to the SWISS-PROT data bank.			
CC	-1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLLOCATION			
CC	OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE			
CC	RIBOSOME (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.			
CC	EF-G/EF-2 SUBFAMILY.			
CC	-----			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: AE006493; AK3347.1; -.			P32257 Kluyveromyc
DR	InterPro: IPR000640; EFG_C.			P25302 saccharomyc
DR	InterPro: IPR000795; GTP_EFTU.			P75471 mycoplasma
DR	InterPro: IPR004161; GTP_EFTU_D2.			P08544 t genome po
DR	Pfam: PF006079; EFG_C. 1.			P08545 t genome po
DR	Pfam: PF000009; GTP_EFTU. 1.			Q01901 p genome po
DR	Pfam: PF03144; GTP_EFTU_D2. 1.			Q50647 mycobacteri
DR	PRINTS: PR00315; ELONGATNFCF.			P80868 bacillus su
DR	PROSITE: PS00301; EFACOR_GTP. 1.			Q93166 chlamydia m
DR	Elongation factor; Protein biosynthesis; GTP-binding;			O84444 chlamydia t
DR				P13550 spirulina p
DR				P43925 haemophilus

KW Complete proteome.  
 FT INT\_MET 0  
 FT NP\_BIND 16 23 GTP (BY SIMILARITY).  
 FT NP\_BIND 80 84 GTP (BY SIMILARITY).  
 FT NP\_BIND 134 137 GTP (BY SIMILARITY).  
 SQ SEQUENCE 691 AA; 76397 MW; D59B857A2CDB40CD CRC64;

Query Match 53.9%; Score 48; DB 1; Length 691;  
 Best Local Similarity 40.0%; Pred. No. 1.9;  
 Matches 6; Conservative 8; Mismatches 1; Indels 0; Gaps 0;

Oy 1 LQTPQLQVMEPQ 15  
 Db 399 IEVPEVQLMEPEK 413

RESULT 2  
 ID TERM\_UREUR STANDARD; PRT; 639 AA.  
 AC P09757;  
 DT 01-MAR-1989 (Rel. 10, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tetracycline resistance protein tetM.  
 GN TEM.  
 OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;  
 OC Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=2130;  
 RN [1]  
 RP SEQUENCE FROM N. A.  
 RA MEDLINE=88144009; PubMed=3344217;  
 RX Sanchez-Pescador R., Brown J.T., Roberts M., Urdea M.S.;  
 RT "The nucleotide sequence of the tetracycline resistance determinant  
 tetM from Ureaplasma urealyticum."  
 RL Nucleic Acids Res. 16:1216-1217(1988).  
 CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN  
 CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.  
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC TEM/ETO SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U08812; AAA73978.1; -.  
 DR PIR; S03268; S03268.  
 DR HSSP; P13551; IFNM.  
 DR InterPro: IPR000640; EFG\_C.  
 DR InterPro: IPR000795; GTP\_EFTU.  
 DR InterPro: IPR004161; GTP\_EFTU\_D2.  
 DR Pfam; PF00679; EFG\_C; 1.  
 DR Pfam; PF00009; GTP\_EFTU; 1.  
 DR Pfam; PF03144; GTP\_EFTU\_D2; 1.  
 DR PRINTS; PR00315; ELONGATNCT.  
 DR PROSITE; PS00301; EFACOR\_GTP; 1.  
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding.  
 FT NP\_BIND 10 17 GTP (BY SIMILARITY).  
 FT NP\_BIND 74 78 GTP (BY SIMILARITY).  
 FT NP\_BIND 128 131 GTP (BY SIMILARITY).  
 SQ SEQUENCE 639 AA; 72599 MW; A1497055BB182B3A CRC64;

Query Match 51.7%; Score 46; DB 1; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 3.8;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 1 LQTPQLQVMEP 14

Db 339 IEVPEVQLMEPEK 352

RESULT 3  
 ID SYUB\_BOVIN STANDARD; PRT; 134 AA.  
 AC P33567;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Beta-synuclein (Phosphonucleoprotein 14) (PMP 14) (14 kDa brain-  
 DE specific protein).  
 GN SNCB.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=94039126; PubMed=823629;  
 RA Nakajo S., Tsukada K., Omata K., Nakamura Y., Nakaya K.;  
 RT "A new brain-specific 14-kDa protein is a phosphoprotein. Its  
 RT complete amino acid sequence and evidence for phosphorylation."  
 RL Eur. J. Biochem. 217:1057-1063(1993).  
 RN [2]  
 RP PARTIAL SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=91038084; PubMed=2230807;  
 RA Nakajo S., Omata K., Aichi T., Shibayama T., Okahashi I., Ochiai H.,  
 RA Nakai Y., Nakaya K., Nakamura Y.;  
 RT "Purification and characterization of a novel brain-specific 14-kDa  
 RT protein."  
 RL J. Neurochem. 55:2031-2038(1990).  
 CC -1- FUNCTION: MAY BE INVOLVED IN NEURONAL PLASTICITY.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: SPECIFICALLY PRESENT IN SYNAPSES AROUND  
 CC NEURONS BUT NOT IN GLIAL CELLS.  
 CC -1- PTM: PHOSPHORYLATED. PHOSPHORYLATION BY G-PROTEIN COUPLED RECEPTOR  
 CC KINASES (GKR) IS MORE EFFICIENT THAN PHOSPHORYLATION BY CK1, CK2  
 CC AND CAM-KINASE II (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE SYNUCLEIN FAMILY.  
 CC -----  
 DR PIR; A60218; A60218.  
 DR PIR; J00238; J00238.  
 DR PIR; S39046; S39046.  
 DR InterPro: IPR001058; Synuclein.  
 DR Pfam; PF01387; Synuclein; 1.  
 DR PRINTS; PR01211; SYNUCLEIN.  
 DR ProDom; PD010631; Synuclein; 1.  
 KW Phosphorylation; Repeat.  
 FT DOMAIN 20 67  
 FT REPEAT 20 30  
 FT REPEAT 31 41  
 FT REPEAT 42 56  
 FT REPEAT 57 67  
 FT MOD\_RES 118 118  
 SQ SEQUENCE 134 AA; 14277 MW; 484FA01A01979966 CRC64;

Query Match 49.4%; Score 44; DB 1; Length 134;  
 Best Local Similarity 46.2%; Pred. No. 1.5;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Oy 5 QPLQVMEPEQD 17  
 Db 105 EPLIEPLMEPEGE 117

RESULT 4



	SYUB	HUMAN		
ID	SVYB	HUMAN	STANDARD;	PRT; 134 AA.
AC	Q16143;			
DT	01-NOV-1997	(Rel. 35,	Created)	
D7	01-NOV-1997	(Rel. 35,	Last sequence update)	
D7	16-OCT-2001	(Rel. 40,	Last annotation update)	
DE	Beta-synuclein.			
GN	SNCB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=94252398; PubMed=8194594;			
RA	Jakes R., Spillantini M.G., Goedert M.;			
RL	"Identification of two distinct synucleins from human brain.";			
RN	FEBS Lett. 345:27-32(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99026142; PubMed=9806846;			
RA	Lavedan C., Leroy E., Torres R., Dehejia A., Dutra A., Buchholz S.,			
RM	Nussbaum R.L., Polymeropoulos M.H.;			
RT	"Genomic organization and expression of the human beta-synuclein gene			
RT	(SNCB).";			
RL	Genomics 54:173-175(1998).			
RN	[3]			
RP	PHOSPHORYLATION.			
RX	MEDLINE=20409007; PubMed=10852916;			
RA	Proulx A.N., Morris A.J., Surguchov A., Benovic J.L.;			
RT	"Synucleins are a novel class of substrates for G protein-coupled			
RT	receptor kinases.";			
RL	J. Biol. Chem. 275:26515-26522(2000).			
CC	-I- FUNCTION: MAY BE INVOLVED IN NEURONAL PLASTICITY.			
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-I- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN; CONCENTRATED			
CC	IN PRESYNAPTIC NERVE TERMINALS.			
CC	-I- PPM: PHOSPHORYLATED. PHOSPHORYLATION BY G-PROTEIN COUPLED RECEPTOR			
CC	KINASES (GKR) IS MORE EFFICIENT THAN PHOSPHORYLATION BY CK1, CK2			
CC	AND CAM-KINSE II.			
CC	-I- DISEASE: BRAIN IRON ACCUMULATION TYPE 1 (NBIA), ALSO CALLED			
CC	HALLEKOVODEN-SPEITZ SYNDROME), A RARE NEUROAXONAL DYSTROPHY, IS			
CC	HISTOLOGICALLY CHARACTERIZED BY AXONAL SPHEROIDS, IRON DEPOSITION,			
CC	LEMNY BODY (LB)-LIKE INTRANEURONL INCLUSIONS, GLIAL INCLUSIONS AND			
CC	NEUROFIBILLARY TANGLAS. SNCB IS FOUND IN SPHEROIDS BUT NOT IN			
CC	INCLUSIONS.			
CC	-I- SIMILARITY: BELONGS TO THE SYNUCLEIN FAMILY.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; S69965; AAB30860.1; -			
DR	EMBL; AF053136; AAC80286.1; -			
DR	EMBL; AF053134; AAC80286.1; JOINED.			
DR	EMBL; AF053135; AAC80286.1; JOINED.			
DR	MIM; 602569; -			
DR	InterPro; IPR001058; Synuclein.			
DR	pfam; PF01387; Synuclein.1			
DR	PRINTS; PR01211; STRUCLEIN.			
DR	ProDom; PD010631; Synuclein; 1.			
KW	Phosphorylation; Repeat.			
FT	DOMAIN	20	67	
FT				4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-R-K-
FT	REPEAT	20	30	[EQ]-[QG]-V-X(4).
FT	REPEAT	31	41	1.
FT	REPEAT	42	56	2.
FT	REPEAT	57	67	3 (APPROXIMATE).
FT	REPEAT			4.

FT	MOD_RES	118	118	PHOSPHORYLATION (BY CK2, GRR2 AND GRR5).
SQ	SEQUENCE	134 AA;	14288 MW;	5BCA9FC6A15AC4EF CRC64;
	Query Match	49.4%;	Score 44;	DB 1;
	Best Local Similarity	46.2%;	Pred. No. 1.5;	
	Matches	6;	Conservative	6;
			Mismatches	1;
			Indels	0;
			Gaps	0;
OY	5 OPLLOWMEPOGD	17		
	::: :: :: :			
Db	105 EPLIEPLMEPEGE	117		
RESULT	5			
STUB_RAT	STANDARD:	PRT,	137 AA.	
AC	Q63754;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Beta-synuclein (Phosphonucleoprotein 14) (PMP 14).			
GN	SNB.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.			
RC	TISSUE=Brain;			
RX	MEDLINE=93019240; PubMed=1402909;			
RA	Tobes T., Nakajo S., Tanaka A., Mitoysa A., Omata K., Nakaya K.,			
RA	Tomita M., Nakamura Y.;			
RT	"Cloning and characterization of the cDNA encoding a novel brain-			
RT	specific 14-kDa protein.";			
RL	J. Neurochem. 59:1624-1629(1992).			
RN	[2]			
RP	PHOSPHORYLATION BY CAM-KINASE II.			
RX	MEDLINE=94039126; PubMed=8223629;			
RA	Nakajo S., Tsukada K., Omata K., Nakamura Y., Nakaya K.;			
RT	"A new brain-specific 14-kDa protein is a phosphoprotein. Its complete			
RT	amino acid sequence and evidence for phosphorylation.";			
RL	Eur. J. Biochem. 217:1057-1063(1993).			
CC	-I- FUNCTION: MAY BE INVOLVED IN NEURONAL PLASTICITY.			
CC	-I- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN BRAIN.			
CC	-I- PFM: PHOSPHORYLATED. PHOSPHORYLATION BY G-PROTEIN COUPLED RECEPTOR			
CC	KINASES (GKR) IS MORE EFFICIENT THAN PHOSPHORYLATION BY CK1, CK2			
CC	AND CAM-KINASE II.			
CC	-I- SIMILARITY: BELONGS TO THE SYNUCLEIN FAMILY.			
CC				
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC				
DR	EMBL, D17764; BAA04610.1; -			
DR	InterPro: IPR001058; Synuclein.			
DR	Pfam: PF01387; Synuclein; 1.			
DR	PRINTS: PR01211; SYNUCLEIN.			
DR	Prodom: PD010631; Synuclein; 1.			
KW	Phosphorylation; Repeat.			
FT	DOMAIN	20	67	
FT				4 X 11 AA TANDEM REPEATS OF [EGS]-K-T-K-
FT	REPEAT	20	30	[EQ]-[GQ]-V-X(4).
FT	REPEAT	31	41	1.
FT	REPEAT	42	56	2.
FT	REPEAT	57	67	3 (APPROXIMATE).
FT	MOD_RES	118	118	4.
FT				PHOSPHORYLATION (BY CK2, GRR2 AND GRR5)
FT				(BY SIMILARITY).
SQ	SEQUENCE	137 AA;	14504 MW;	67BC6CB84FA01A03 CRC64;

Query Match 49.4%; Score 44; DB 1; Length 137;  
 Best Local Similarity 46.2%; Pred. No. 1.5;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 QPILQVMEPEGD 17  
 :||:|||||:  
 DB 105 EPLIEPLEPEGE 117

RESULT 6  
 TET9\_ENTFA STANDARD; PRT; 639 AA.  
 ID TET9\_ENTFA  
 AC P21598;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tetracycline resistance protein tetM from transposon Tn916  
 DE (tetM(916)).  
 GN TETM OR TET(M).  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;  
 OC Enterococcus.  
 OC NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TRANSPOSON-Tn916;  
 RX MEDLINE=91045089; PubMed=2172929;  
 RA Burdett V.;  
 RT "Nucleotide sequence of the tet(M) gene of Tn916."  
 RL Nucleic Acids Res. 18:6137-6137(1990).  
 CC - FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN  
 CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.  
 CC - SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC TETM/TETO SUBFAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL: X56353; CAA39796.1; -  
 CC DR PIR: S13142; S13142.  
 CC DR HSSP: P13551; 1FNM.  
 CC DR InterPro: IPR000640; EFG\_C.  
 CC DR InterPro: IPR000795; GTP\_EFTU.  
 CC DR InterPro: IPR004161; GTP\_EFTU\_D2.  
 CC DR Pfam: PF00679; EFG\_C; 1.  
 CC DR Pfam: PF00009; GTP\_EFTU; 1.  
 CC DR Pfam: PF03144; GTP\_EFTU\_D2; 1.  
 CC DR PRINTS: PR00315; ELONGATNFC.  
 CC DR PROSITE: PS00301; EFACOR\_GTP; 1.  
 CC KW Protein biosynthesis; Antibiotic resistance; GTP-binding;  
 CC TM Transposable element.  
 CC FT NP\_BIND 10 17 GTP (BY SIMILARITY).  
 CC FT NP\_BIND 74 78 GTP (BY SIMILARITY).  
 CC FT NP\_BIND 128 131 GTP (BY SIMILARITY).  
 CC SQ SEQUENCE 639 AA; 72464 MW; B2315A37B53B18FB CRC64;

Query Match 48.3%; Score 43; DB 1; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQTPQLQVMEP 14  
 :|||:|:  
 DB 339 IENHPPLQTVEP 352

RESULT 7

TETM\_STAUB STANDARD; PRT; 639 AA.  
 ID TETM\_STAUB  
 AC Q53770;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Tetracycline resistance protein tetM (tetM(M)).  
 GN TETM OR TET(M).  
 OS Staphylococcus aureus.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Staphylococcus.  
 OC NCBI\_TaxID=1280;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91158314; PubMed=2073121;  
 RA Nesin M., Svec P., Lupski J.R., Godson G.N., Kreiswirth B.,  
 RA Projan S.J.;  
 RT "Cloning and nucleotide sequence of a chromosomally encoded  
 RT tetracycline resistance determinant, tet(M), from a pathogenic,  
 RT methicillin-resistant strain of staphylococcus aureus."  
 RL Antimicrob. Agents Chemother. 34:2273-2276(1990).  
 CC - FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN  
 CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.  
 CC - SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.  
 CC TETM/TETO SUBFAMILY.  
 CC -----  
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 CC -----  
 CC DR EMBL: M21136; AA26678.1; -  
 CC DR HSSP: P13551; 1FNM.  
 CC DR InterPro: IPR000640; EFG\_C.  
 CC DR InterPro: IPR000795; GTP\_EFTU.  
 CC DR InterPro: IPR004161; GTP\_EFTU\_D2.  
 CC DR Pfam: PF00679; EFG\_C; 1.  
 CC DR Pfam: PF00009; GTP\_EFTU; 1.  
 CC DR Pfam: PF03144; GTP\_EFTU\_D2; 1.  
 CC DR PRINTS: PR00315; ELONGATNFC.  
 CC DR PROSITE: PS00301; EFACOR\_GTP; 1.  
 CC KW Protein biosynthesis; Antibiotic resistance; GTP-binding;  
 CC TM Transposable element.  
 CC FT NP\_BIND 10 17 GTP (BY SIMILARITY).  
 CC FT NP\_BIND 74 78 GTP (BY SIMILARITY).  
 CC FT NP\_BIND 128 131 GTP (BY SIMILARITY).  
 CC SQ SEQUENCE 639 AA; 72639 MW; 66470062A673BE1F CRC64;

Query Match 48.3%; Score 43; DB 1; Length 639;  
 Best Local Similarity 50.0%; Pred. No. 12;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQTPQLQVMEP 14  
 :|||:|:  
 DB 339 IENHPPLQTVEP 352

RESULT 8  
 EFG\_AGRU STANDARD; PRT; 699 AA.  
 ID EFG\_AGRU  
 AC P70782;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Elongation factor G (EF-G).  
 GN FUS\_A.  
 OS Agrobacterium tumefaciens.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
 OC Rhizobiaceae; Rhizobium.  
 OC NCBI\_TaxID=358;

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97047977; PubMed-8892818;
RA Syvonen A., Amiri H., Jamel A., Andersson S.G.E., Kurland C.G.;
RT "A chimeric disposition of the elongation factor genes in Rickettsia
   prowazekii."
RL J. Bacteriol. 178:6192-6199(1996).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION
   OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
   RIBOSOME.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
   EF-G/EF-2 SUBFAMILY.
CC -----
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CC -----
DR EMBL: X96673; CAAG7990.1; -.
DR HSSP: P13551; 1FNM.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam: PF00679; EFG_C.1.
DR Pfam: PF00009; GTP_EFTU.1.
DR Pfam: PF03144; GTP_EFTU_D2.1.
DR PROSITE: PS00301; EFACITOR_GTP.1.
KM Elongation factor; Protein biosynthesis; GTP-binding.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 86 90 GTP (BY SIMILARITY).
FT NP_BIND 140 143 GTP (BY SIMILARITY).
SQ SEQUENCE 699 AA; 78044 MW; E72A1081DEC28E2B CRC64;

Query Match
Best Local Similarity 48.3%; Score 43; DB 1; Length 699;
Matches 7; Conservative 8; Mismatches 2; Indels 2; Gaps 1;

OY 1 LQTPQLQVMMEP--QGD 17
DB 406 MEPEVIOIAIEPKTKGD 424

RESULT 9
VP40_HSV2
ID VP40_HSV2 STANDARD; PRT; 643 AA.
AC P52369;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Capsid protein P40 [Contains: Assemblin (Protease) (EC 3.4.21.97);
   DE Capsid assembly protein].
GN 17
OS Equine herpesvirus type 2 (strain 86/87) (EHV-2).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae.
OX NCBI_TaxID=82831;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-95302501; PubMed-7783207;
RA Telford E.A., Watson M.S., Aird H.C., Perry J., Davison A.J.;
RT "The DNA sequence of equine herpesvirus 2."
RL J. Mol. Biol. 249:520-528(1995).
CC -1- FUNCTION: THE CAPSID ASSEMBLY PROTEIN IS COMPONENT OF THE CAPSID
   CORE INVOLVED IN PROCESSING AND PACKAGING OF PROGENY DNA.
CC -1- FUNCTION: ASSEMBLIN IS A PROTEASE WHICH CAN PROTEOLYTICALLY CLEAVE
   ITSELF AND THE CAPSID ASSEMBLY PROTEIN AT THE C-TERMINUS.
CC -1- CATALYTIC ACTIVITY: PREFERENTIALLY CLEAVES AT ALA-I-SER OR ALA-I-
   ALA.

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CC -1- CATALYTIC ACTIVITY: CLEAVES -ALA + SER- AND -ALA + ALA- BONDS IN
   THE SCAFFOLD PROTEIN.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S21 (SERINE PROTEASE).
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.
CC -----
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CC -----
DR EMBL: U20824; AAC13804.1; -.
DR HSSP: P16753; 1CMV.
DR MEROPS: S21.001; -.
DR InterPro: IPR001847; Assemblin.
DR Pfam: PF00716; Peptidase_S21.1.
KM Coat protein; Hydrolyase; Serine protease.
FT CHAIN 1 269 ASSEMBLIN (PROTEASE).
FT CHAIN 270 643 CAPSID ASSEMBLY PROTEIN.
FT SITE 269 270 CLEAVAGE (BY THE PROTEASE) (PROBABLE).
FT ACT_SITE 82 82 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 173 173 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 643 AA; 68394 MW; 1108A7A40E9FCA38 CRC64;

Query Match
Best Local Similarity 47.2%; Score 42; DB 1; Length 643;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 2 QTPQLQVMMERQ 15
DB 486 QEPQPLQPOLQ 499

RESULT 10
YHGC_ECOLI
ID YHGC_ECOLI STANDARD; PRT; 78 AA.
AC P46845;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yhgc.
GN YHGC OR B3410 OR Z4765 OR EC54252.
OS Escherichia coli, and
OC Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
   RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
   RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
   RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE-21074935; PubMed-11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
   RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
   RA Fostel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
   RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
   RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
   RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
RL Nature 409:529-533(2001).

```

RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-0157.H7 / RIMD 0509952;  
 RX MEDLINE-21156231; PubMed-11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K.,  
 Han C.-G., Ohtsubo H., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 Kihara S., Shiba T., Hattori M., Shinagawa H.;  
 RT Complete genome sequence of enterohemorrhagic *Escherichia coli*  
 O157:H7 and genomic comparison with a laboratory strain K-12.\*;  
 RL DNA Res. 8:11-22(2001).  
 CC -----  
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 CC -----  
 CC EMBL: U18997; AAC58208.1; -;  
 DR EMBL: AE000416; AAC76435.1; -;  
 DR EMBL: AE005563; AAG58511.1; -;  
 DR EMBL: AP002565; BAB37675.1; -;  
 DR ECGene: EGI29333; yhgC.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 78 AA; 8660 MW; 8897bDE22CA9024B CRC64;

Query Match 46.1%; Score 41; DB 1; Length 78;  
 Best Local Similarity 46.2%; Pred. No. 2.6;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 LGTPOPLQVME 13  
 Db 26 LMTPOPMINAMLO 38

RESULT 11  
 TCGP\_DROME STANDARD; PRT; 544 AA.  
 AC P48605; O9VER9;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE T-complex protein 1, gamma subunit (TCP-1-gamma) (CCT-gamma).  
 GN CCT-GAMMA OR CCT-3 OR CCG OR CG8977.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Phryganea; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-CANTON-S.  
 RA Martin C.H., Mayeda C.A., Davis C.A., Ericsson C.L., Kafets J.D.,  
 Mathog D.R., Celinker S.E., Lewis E.B., Palazzolo M.J.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-96257223; PubMed-8666276;  
 RA Walkley N.A., Malik A.N.;  
 RT "Drosophila melanogaster P1 genomic clone DS05563 contains the  
 RL chaparrin-encoding gene Ccgc.";  
 RL Gene 171:221-223(1996).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 Abell J.F., Adyanthi A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,  
 Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 Burks K.C., Busam D.A., Butler H., Cadieu E., Canter A., Chandra I.,  
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,  
 Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,  
 Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshire A.,  
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 Sytkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,  
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 CC -1- FUNCTION: MOLECULAR CHAPERONE; ASSIST THE FOLDING OF PROTEINS UPON  
 CC ATP HYDROLYSIS. KNOWN TO PLAY A ROLE, IN VITRO, IN THE FOLDING OF  
 CC ACTIN AND TUBULIN.  
 CC -1- SUBUNIT: HETERO-OLIGOMERIC COMPLEX OF ABOUT 850 TO 900 kDa THAT  
 CC FORMS TWO STACKED RINGS, 12 TO 16 NM IN DIAMETER.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO THE TCP-1 CHAPERONIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U31961; AAC44416.1; -;  
 DR EMBL: X95602; CAA64860.1; -;  
 DR EMBL: AE003714; AAF55350.1; -;  
 DR HSSP: P48424; 1A6D.  
 DR FlyBase: FBgn0015019; Cct-gamma.  
 DR InterPro: IPR002423; TCP1\_cpn60.  
 DR InterPro: IPR002194; TCP\_1.  
 DR Pfam: PF00118; cpn60\_TCP1\_1.  
 DR PRINTS: PR00304; TCOMPLEXTCP1.  
 DR PROSITE: PS00750; TCP1\_1; 1.  
 DR PROSITE: PS00751; TCP1\_2; 1.  
 DR PROSITE: PS00995; TCP1\_3; 1.  
 KW Chaperone; ATP-binding; Multigene family.  
 FT CONFLICT 12 12 S -> SD (IN REF. 2).  
 FT CONFLICT 35 47 MISSING (IN REF. 1).  
 SQ SEQUENCE 544 AA; 59394 MW; DD5E635809B322C2 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 544;  
 Best Local Similarity 46.2%; Pred. No. 22;  
 Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 PPLQVMEPPG 16

DB 44 POAMLKMLMDPMWG 56

```

RESULT 12
TETS_ENTFA STANDARD: PRT: 639 AA.
ID TETS_ENTFA P1131:
AC 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tetracycline resistance protein tetM from transposon Tn1545
DE (TetM(1545)).
DE TETM OR TET(M).
GN Enterococcus faecalis (Streptococcus faecalis).
OS Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BM4127; TRANSPOSON-Tn1545;
RX MEDLINE=87016342; PubMed=3020504;
RA Martin P., Trieu-Cuot P., Courvalin P.;
RT "Nucleotide sequence of the tetM tetracycline resistance determinant
of the streptococcal conjugative shuttle transposon Tn1545.";
RL Nucleic Acids Res. 14:7047-7058(1986).
CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN
SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC TETM/TETO SUBFAMILY.
CC -----
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CC -----
DR EMBL: X04388; CAN27977.1; -
DR PIR: A24333; A24333.
DR HSSP: P1351; IFNM.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam: PF00679; EFG_C; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATNFCF.
DR PROSITE: PS00301; EFACOR_GTP; 1.
KW Protein biosynthesis; Antibiotic resistance; GTP-binding;
KW Transposable element.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 74 78 GTP (BY SIMILARITY).
FT NP_BIND 128 131 GTP (BY SIMILARITY).
SQ SEQUENCE 639 AA; 72657 MW; 2F7A3CD0588253CE CRC64;

Query Match 46.1%; Score 41; DB 1; Length 639;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LGTPOPLQVMMEP 14
DB 339 IENPLPLQTVYEP 352

```

```

DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Tetracycline resistance protein tetM from transposon Tn5251 (Tet(M)).
GN TETM(5251).
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DP 1322;
RX MEDLINE=96162866; PubMed=8595862;
RA Provvedi R., Manganello R., Pozzi G.;
RT "Characterization of conjugative transposon Tn5251 of Streptococcus
pneumoniae.";
RL FEMS Microbiol. Lett. 135:231-236(1996).
CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN
SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC TETM/TETO SUBFAMILY.
CC -----
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CC -----
DR EMBL: X90939; CAN62436.1; -
DR HSSP: P1351; IFNM.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam: PF00679; EFG_C; 1.
DR Pfam: PF00009; GTP_EFTU; 1.
DR Pfam: PF03144; GTP_EFTU_D2; 1.
DR PRINTS: PR00315; ELONGATNFCF.
DR PROSITE: PS00301; EFACOR_GTP; 1.
KW Protein biosynthesis; Antibiotic resistance; GTP-binding;
KW Transposable element.
FT NP_BIND 10 17 GTP (BY SIMILARITY).
FT NP_BIND 74 78 GTP (BY SIMILARITY).
FT NP_BIND 128 131 GTP (BY SIMILARITY).
SQ SEQUENCE 639 AA; 72556 MW; F18131E0881F3C0 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 639;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LGTPOPLQVMMEP 14
DB 339 IENPLPLQTVYEP 352

RESULT 14
TETS_LISMO STANDARD: PRT: 641 AA.
AC 048791;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Tetracycline resistance protein tets (Tet(S)).
GN TETS OR TET(S).
OS Listeria monocytogenes.
OG Plasmid p18811.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BM4210;
RX MEDLINE=93380670; PubMed=8370538;

```

```

RA  Charpentier E., Gerpaud G., Courvalin P.: tetracycline-resistance gene
RT  "Characterization of a new class of tetracycline-resistance gene
RL  tet(S) in Listeria monocytogenes BM4210." ;
CC  Gene J11:27-34(1993).
CC  -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN
CC  SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.
CC  -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC  TERM/TEO SUBFAMILY.
-----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; L09756; AAA25293.1; -.
DR  HSSP; P13551; IFNM.
DR  InterPro; IPR000640; EFG_C.
DR  InterPro; IPR000795; GTP_EFTU.
DR  InterPro; IPR004161; GTP_EFTU_D2.
DR  Pfam; PF00679; EFG_C.1.
DR  Pfam; PF00009; GTP_EFTU.1.
DR  Pfam; PF03144; GTP_EFTU_D2.1.
DR  PRINTS; PR00315; ELONGATNFCT.
DR  PROSITE; PS00301; EFACITOR_GTP.1.
DR  Protein biosynthesis; Antibiotic resistance; GTP-binding; Plasmid.
KW  NP_BIND 10 17 GTP (BY SIMILARITY).
FT  NP_BIND 74 78 GTP (BY SIMILARITY).
FT  NP_BIND 128 131 GTP (BY SIMILARITY).
SQ  SEQUENCE 641 AA; 73014 MW; EC534FD38FD54FC2 CRC64;

Query Match 46.1%; Score 41; DB 1; Length 641;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 LOTPQLQVMMEP 14
   I I I I I I I I
DB 339 LENPLPMQTTEP 352

RESULT 15
TETS_LACIA STANDARD; PRT; 646 AA.
ID TETS_LACIA
AC 048712;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tetracycline resistance protein tets (Tet(S)).
GN TETS OR TET(S).
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OG Plasmid pK214.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
CC Lactococcus.
OX NCBI_TaxID=1360;
RX [1]
RP SEQUENCE FROM N.A.
RN STRAIN=K214;
RA Perleth V., Schwarz F., Cresta L., Boeglin M., Dasen G., Teuber M.;
RL "Antibiotic resistance spread in food.";
CC Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ABOLISH THE INHIBITORY EFFECT OF TETRACYCLIN ON PROTEIN
CC SYNTHESIS BY A NON-COVALENT MODIFICATION OF THE RIBOSOMES.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC TERM/TEO SUBFAMILY.
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CC -----
DR EMBL: X92846: CAA63528.1; -.
DR HSSP: P13551: IFNM.
DR InterPro: IPR000640: EFG_C.
DR InterPro: IPR000795: GTP_EFTU.
DR InterPro: IPR004161: GTP_EFTU_D2.
DR Pfam: PF00679: EFG_C; 1.
DR Pfam: PF00009: GTP_EFTU; 1.
DR Pfam: PF03144: GTP_EFTU_D2; 1.
DR PRINTS: PR00315: ELONGACTNCT.
DR PROSITE: PS00301: EFACFOR_GTP; 1.
FW Protein biosynthesis: Antibiotic resistance: GTP-Binding: Plasmid.
KW NP_BIND 15 22 GTP (BY SIMILARITY).
FT NP_BIND 79 83 GTP (BY SIMILARITY).
ET NP_BIND 133 136 GTP (BY SIMILARITY).
SO SEQUENCE 646 AA: 73711 MW: 135513BA2F644BB6 CAC64;
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Query Match	46.1%;	Score 41;	DB 1;	length 646;
Best Local Similarity	50.0%;	Score No. 27;		
Matches	7;	Conservative	3;	Mismatches 4;
				Indels 0;
				Gaps 0;
QY	1	LQTPQLQVMMEP	14	
		:   :   :   :		
Db	344	LENPLMLQTTIEP	357	

Search completed: July 31, 2002, 15:27:16  
Job time: 209 sec









Db 415 IEVPEVYQLVMEPK 429

RESULT 2

0928G4 PRELIMINARY; PRT; 192 AA.

AC 0928G4; (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE LIN2571. PROTEIN.

GN LIN2571.

OS Listeria innocua.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Listeria.

OX NCBI\_TaxID=1642;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CLIP 11262 / SEROVAR 6A;

RX PubMed-11679669;

RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Cherouani F., Couve E., de Darvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurge O.,

RA Entian K.-D., Eschl H., Garcia-del Portillo F., Garrido P.,

RA Gautier L., Goebel U., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

RA Jones L.-M., Kreft J., Kunst F., Kurapik G.,

RA Madueno E., Malouin A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordsted G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,

RA Rammel B., Rose M., Schluter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

RT "Comparative genomics of Listeria species."

RL Science 294:849-852(2001).

DR EMBL: AL596172; CAC97798.1;

DR Listlist: LIN02571;

KW Complete proteome.

SQ SEQUENCE 192 AA; 20841 MW; BEBA4BD3261DDA74 CRC64;

Query Match 53.4%; Score 47.5; DB 16; Length 192;

Best Local Similarity 50.0%; Pred. No. 3.5;

Matches 9; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

OY 3 TPQPL---LOYMPEQD 17

Db 31 TPKPLPGVEISVPEQD 48

RESULT 3

097503 PRELIMINARY; PRT; 693 AA.

AC 097503; (TREMBlrel. 18, Created)

DT 01-DEC-2001 (TREMBlrel. 18, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TRANSLATION ELONGATION FACTOR G.

GN SP0273.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

OX NCBI\_TaxID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-TIGR4;

RC MEDLINE-21357209; PubMed-11463916;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,

RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Raddue D.,

RA Holtzapfe E., Khouri H., Wolf A.M., Uitterback T.R., Hansen C.L.,

RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickenson T., Hickey E.K.,

RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

RT "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae."

RT Science 293:498-506(2001).

DR EMBL: AE007340; AKK74451.1;

DR TIGR: SP0273;

DR InterPro: IPR000640; EFG\_C.

DR InterPro: IPR000795; GTP\_EFTU.

DR InterPro: IPR004161; GTP\_EFTU\_D2.

DR Pfam: PF00679; EFG\_C. 1.

DR Pfam: PF00009; GTP\_EFTU. 1.

DR Pfam: PF03144; GTP\_EFTU\_D2. 1.

DR PRINTS: PR00315; ELONGINFCT.

DR PROSITE: PS00301; EFCTOR\_GTP. 1.

KW Elongation factor; Complete proteome.

SQ SEQUENCE 693 AA; 76831 MW; 73187D0287AC6193 CRC64;

Query Match 51.7%; Score 46; DB 16; Length 693;

Best Local Similarity 40.0%; Pred. No. 23;

Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 LQTPQPLLOYMPEQ 15

Db 400 INVEPEVYQLVMEPK 414

RESULT 4

035745 PRELIMINARY; PRT; 667 AA.

AC 035745; (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-JAN-1998 (TREMBlrel. 19, Last annotation update)

DE ZINC FINGER PROTEIN REGULATOR OF APOPTOSIS AND CELL CYCLE ARREST.

GN ZAC1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-PITUITARY GLAND;

RC MEDLINE-97327559; PubMed-9184226;

RA Spengler D., Villalba M., Hoffmann A., Pantalon C., Housseini S.,

RA Bockaert J., Journot L.,

RT "Regulation of apoptosis and cell cycle arrest by Zac1, a novel zinc finger protein expressed in the pituitary gland and the brain."

RL EMBO J. 16:2814-2825(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BALB/C; TISSUE-PITUITARY GLAND;

RA Spengler D., Villalba M., Hoffmann A., Pantalon C., Housseini S.,

RA Bockaert J., Journot L.,

CC Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).

DR EMBL: X95503; CAA64757.1;

DR EMBL: X95504; CAA64758.1;

DR MGD: MGI:1100874; Zac1.

DR InterPro: IPR000823; ZnF-C2H2.

DR Pfam: PF00096; zf-C2H2. 7.

DR PRINTS: PR00048; ZNCFINGER.

DR SMART: SM00355; ZnF\_C2H2. 7.

DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 7.

DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.

KW DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.

SQ SEQUENCE 667 AA; 75258 MW; 392F0AC979C8C10F CRC64;

Query Match 50.6%; Score 45; DB 11; Length 667;

Best Local Similarity 60.0%; Pred. No. 32;

Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 LQTPQPLLOYMPEQ 15

Db 543 LPVQPLPQPOMQPQ 557

## RESULT 5

Q9EPT3 PRELIMINARY; PRT; 675 AA.  
 AC Q9EPT3; 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE LOST ON TRANSFORMATION PROTEIN 1.  
 GN ZAC1 OR LOT1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RX STRAIN=NIH-SWISS;  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20065118; PubMed=10597250;  
 RA Abdollahi A., Bao R., Hamilton T.C.;  
 RT "LOT1 is a growth suppressor gene down-regulated by the epidermal  
 growth factor receptor ligands and encodes a nuclear zinc-finger  
 protein.";  
 RT Oncogene 18:6477-6487(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NIH-SWISS;  
 RA Abdollahi A., Hamilton T.C.;  
 RT "Identification of a splice variant of mouse Lot1 gene."  
 RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF324471; ANG48331.1;  
 DR MGD: MGI:1100874; Zacl.  
 DR InterPro: IPR000822; Znf-C2H2.  
 DR Pfam: PF00096; Zf-C2H2; 7.  
 DR SMART: SM00355; Znf\_C2H2; 7.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 1.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.  
 DR DNA-binding; Metal-binding; Zinc-finger.  
 KW SEQUENCE 675 AA; 76109 MW; 0F467D165CA5B097 CRC64;

Query Match 50.6%; Score 45; DB 11; Length 675;  
 Best Local Similarity 60.0%; Pred. No. 33;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LQTPQLQVMEPQ 15  
 Db 540 LPVQPLPQPOMQPQ 554

## RESULT 6

Q9JLQ4 PRELIMINARY; PRT; 704 AA.  
 AC Q9JLQ4; 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE ZINC FINGER PROTEIN ZAC1.  
 GN ZAC1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20136063; PubMed=10669760;  
 RA Huang S.-M., Stallcup M.R.;  
 RT "Mouse Zacl, a Transcriptional Coactivator and Repressor for Nuclear  
 Receptors.";  
 RT Mol. Cell. Biol. 20:1855-1867(2000).  
 DR EMBL: AF147785; AAF34245.1; -

DR MGD: MGI:1100874; Zacl.  
 DR InterPro: IPR000822; Znf-C2H2.  
 DR Pfam: PF00096; Zf-C2H2; 7.  
 DR SMART: SM00355; Znf\_C2H2; 7.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 7.  
 DR PROSITE: PS50157; ZINC\_FINGER\_C2H2\_2; 6.  
 DR DNA-binding; Metal-binding; Zinc-finger.  
 KW SEQUENCE 704 AA; 79214 MW; 3AF88262D504FA80 CRC64;

Query Match 50.6%; Score 45; DB 11; Length 704;  
 Best Local Similarity 60.0%; Pred. No. 34;  
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LQTPQLQVMEPQ 15  
 Db 543 LPVQPLPQPOMQPQ 557

## RESULT 7

Q91Z23 PRELIMINARY; PRT; 133 AA.  
 AC Q91Z23; 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE BETA-SYNOCLEIN.  
 GN SNCB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21367613; PubMed=11474193;  
 RA Sopher B.L., Koszidin K.L., McClain M.E., Myrick S.B., Martinez R.A.,  
 RA Smith A.C., La Spada A.R.;  
 RT "Genomic organization, chromosome location, and expression analysis of  
 mouse beta-synuclein, a candidate for involvement in  
 neurodegeneration.";  
 RL Cytogenet. Cell Genet. 93:117-123(2001).  
 DR EMBL: AF348164; AAK83238.1;  
 DR EMBL: AF348162; AAK83238.1; JOINED.  
 DR EMBL: AF348163; AAK83238.1; JOINED.  
 KW SEQUENCE 133 AA; 14052 MW; 8274D8A6AD08EAD5 CRC64;

Query Match 49.4%; Score 44; DB 11; Length 133;  
 Best Local Similarity 46.2%; Pred. No. 9.2;  
 Matches 6; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 5 QPLQVMEPQD 17  
 Db 104 EPLIEPLMEPEGE 116

## RESULT 8

Q90538 PRELIMINARY; PRT; 182 AA.  
 AC Q90538; 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
 DE MEROZOITE SURFACE PROTEIN 1 (FRAGMENT).  
 GN MSP-1.  
 OS Plasmodium vivax.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OC NCBI\_TaxID=5855;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RPV97-73;  
 RA Kim S.H., Kwon S.I.;  
 RT "Analysis of the Plasmodium vivax merozoite surface protein 1 gene

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RT sequence from resurgent Korean isolates."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-KPV97-73;
RA Lee K.N., Song K.J., Song J.W., Lim C.S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF098282; AAF25530.1; -
FT NON_TER 1
FT NON_TER 182
SQ SEQUENCE 182 AA; 19514 MW; 2BB8A7A12D4471C5 CRC64;

Query Match 49.4%; Score 44; DB 5; Length 182;
Best Local Similarity 56.2%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 2 QTPQPLQVMMPEQD 17
Db 56 QQPQSQVVPAPAGD 71

RESULT 9
OQ9N959 PRELIMINARY; PRT; 227 AA.
AC OQ9N959;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE POSSIBLE HYPOTHETICAL 14.6 KDA PROTEIN.
GN CHRL.04.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_Taxid=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TRE0927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerard C., Rajandream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL59782; CAB95318.1; -
SQ SEQUENCE 227 AA; 26099 MW; AAF344E1959DD1E3 CRC64;

Query Match 49.4%; Score 44; DB 5; Length 227;
Best Local Similarity 57.1%; Pred. No. 16;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 QTPQPLQVMMPEQ 15
Db 48 QIPQSVLQVLEPR 61

RESULT 10
OQ9FXA2 PRELIMINARY; PRT; 671 AA.
AC OQ9FXA2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE PUTATIVE POLY-A BINDING PROTEIN.
GN F14J22.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremetskaya I., Kim C., Lenz C., Li J., Liu S.,

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RA Lueros S., Schwartz J., Shin P., Toriumi M., Vysotskaya V.S.,
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Bann J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamuya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC011807; AAG13056.1; -
DR EMBL; AF370517; AAK43894.1; -
DR HSSP; P11940; ICVJ.
DR InterPro: IPR002343; Hud_Sxl_RNA.
DR InterPro: IPR002004; PABP.
DR InterPro: IPR003954; RRM_1.
DR Pfam; PF00658; PABP; 1.
DR PRINTS; SM00517; POLYA. 1.
DR SMART; SM00360; RRM; 4.
DR SMART; SM00361; RRM_1; 4.
DR PROSITE; PS50102; RRM; 4.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
SQ SEQUENCE 671 AA; 72779 MW; 49712E533BD4E55 CRC64;

Query Match 49.4%; Score 44; DB 10; Length 671;
Best Local Similarity 46.7%; Pred. No. 48;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

OY 2 QTPQPLQVMMPEQ 16
Db 514 QQPSPMMQOQMPRG 528

RESULT 11
OQ9S4T6 PRELIMINARY; PRT; 252 AA.
AC OQ9S4T6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TETRACYCLINE RESISTANCE PROTEIN (FRAGMENT).
GN TETM.
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_Taxid=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TRNG 400;
RA Ferreira E., Louro D., Gomes J.P., Catry M.A., Vaz Pato M.V.;
RT "Surveillance of tetracycline-resistant gonococci in Lisbon. Isolation
RT of a TRNG strain with tetracycline MIC=2 mg/L."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF116348; AAD48368.1; -
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam; PF00009; GTP_EFTU; 1.
DR Pfam; PF03144; GTP_EFTU_D2; 1.
KW Cyclin; GTP-binding.
FT NON_TER 1
FT NON_TER 252
SQ SEQUENCE 252 AA; 29007 MW; 25BE46A2F2BDC067 CRC64;

Query Match 48.3%; Score 43; DB 2; Length 252;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 LQTPPLQVMMPE 14  
 Db 234 IENPHPLQTVTP 247

RESULT 12  
 094103

PRELIMINARY; PRT; 472 AA.

AC 094103: PRELIMINARY; PRT; 472 AA.  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE POLYADENYLATED MRNA-BINDING PROTEIN 2 (FRAGMENT).  
 GN PAB2.  
 OS Anemia phyllitidis (Fern).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Filicophyta; Filicopsida; Filicales; Schizaeaceae; Anemia.  
 OX NCBI\_TaxID=12940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Vuorek O., Moepes B., Schraudolf H.;  
 RT "cDNA cloning of poly(A)-binding proteins from fern Anemia  
 phyllitidis."  
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY030359; AAK51123.1; -.  
 FT NON\_TER  
 SQ SEQUENCE 472 AA; 51880 MW; 85499785D003B424 CRC64;

Query Match 48.3%; Score 43; DB 10; Length 472;  
 Best Local Similarity 50.0%; Pred. No. 49;  
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPPLQVMMPEOG 17  
 Db 318 QQPPLMOQMLPRG 338

RESULT 13  
 09M6E4  
 AC 09M6E4: PRELIMINARY; PRT; 479 AA.  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE POLY(A)-BINDING PROTEIN (FRAGMENT).  
 GN PABP.  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Le H., Gallie D.R.;  
 RT "Sequence diversity and conservation of the poly(A)-binding protein in  
 RT plants."  
 RL Plant Sci. 152:101-114(2000).  
 DR EMBL; AF190657; AAF68825.1; -.  
 DR HSSP; P11940; ICVJ.  
 DR InterPro: IPR002004; PABP.  
 DR InterPro: IPR000504; RRM.  
 DR Pfam: PF00658; PABP; 1.  
 DR Pfam: PF00076; rrm; 2.  
 DR SMART; SM00517; POLYA; 1.  
 DR SMART; SM00360; RRM; 2.  
 DR PROSITE; PS50102; RRM; 2.  
 DR PROSITE; PS00030; RRM\_RNP\_1; UNKNOWN\_1.  
 FT NON\_TER  
 SQ SEQUENCE 479 AA; 52626 MW; A2C3F46C3D688A12 CRC64;

Query Match 48.3%; Score 43; DB 10; Length 479;

Best Local Similarity 53.3%; Pred. No. 50;  
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QTPPLQVMMPEOG 16  
 Db 324 QQPPLMOQMLPRG 338

RESULT 14  
 057224

PRELIMINARY; PRT; 639 AA.

AC 057224: PRELIMINARY; PRT; 639 AA.  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE ORF11.  
 GN TET.  
 OS Enterococcus faecalis (Streptococcus faecalis).  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;  
 OC Enterococcus.  
 OX NCBI\_TaxID=1351;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RX MEDLINE-95207419; PubMed-7899523;  
 RA Flanagan S.E., Zitzow L.A., Su Y.A., Clewell D.B.;  
 RT "Nucleotide sequence of the 18-kb conjugative transposon Tn916 from  
 RT Enterococcus faecalis."  
 RL Plasmid 32:350-354(1994).  
 RN [2]  
 RP SEQUENCE OF 636-639 FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RX MEDLINE-94134828; PubMed-8302931;  
 RA Su Y.A., Clewell D.B.;  
 RT "Characterization of the left 4 kb of conjugative transposon Tn916;  
 RT determinants involved in excision."  
 RL Plasmid 30:234-250(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RX MEDLINE-92368175; PubMed-1323953;  
 RA Su Y.A., He P., Clewell D.B.;  
 RT "Characterization of the tet(M) determinant of Tn916: evidence for  
 RT regulation by transcription attenuation."  
 RL Antimicrob. Agents Chemother. 36:769-778(1992).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DS16; TRANSPOSON-TN916;  
 RA Clewell D.B.;  
 RT Submitted (May-1994) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U09422; AAB60022.1; -.  
 DR EMBL; M85225; AAA24784.1; -.  
 DR HSSP; P13551; IFNM.  
 DR InterPro: IPR000640; EFG\_C.  
 DR InterPro: IPR000795; GTP\_EFTU.  
 DR InterPro: IPR004161; GTP\_EFTU\_D2.  
 DR Pfam: PF00679; EFG\_C; 1.  
 DR Pfam: PF00009; GTP\_EFTU; 1.  
 DR Pfam: PF03144; GTP\_EFTU\_D2; 1.  
 DR PRINTS; PR00315; ELONGATNFC.  
 DR PROSITE; PS00301; EFACOR\_GTP; 1.  
 KW GTP-binding.  
 SQ SEQUENCE 639 AA; 72491 MW; D5299DCA60467C3D CRC64;

Query Match 48.3%; Score 43; DB 2; Length 639;

Best Local Similarity 50.0%; Pred. No. 67;  
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQTPPLQVMMPE 14  
 Db 339 IENPHPLQTVTP 352

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RESULT 15
Q9AC90 ID Q9AC90 PRELIMINARY; PRT; 639 AA.
AC Q9AC90;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TET(M).
GN TET(M).
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21220755; PubMed=11320127;
RA "Roberts A.P., Johannesen P.A., Lytras D., Mullany P., Rood J.I.;
RT "Comparison of Tn3397 from Clostridium difficile, Tn916 from
RT Enterococcus faecalis and the CW459let(M) element from Clostridium
RT perfringens shows that they have similar conjugation regions but
RT different insertion and excision modules.";
RL Microbiology 147:1243-1251(2001).
DR EMBL: AE329848; AKI7952.1; -.
DR HSSP: P1351; IDAR.
DR InterPro: IPR000640; EFG_C.
DR InterPro: IPR000795; GTP_EFTU.
DR InterPro: IPR004161; GTP_EFTU_D2.
DR Pfam: PF00679; EFG_C_1.
DR Pfam: PF00009; GTP_EFTU_1.
DR Pfam: PF03144; GTP_EFTU_D2_1.
DR PRINTS: PR00315; ELONGATNFACT.
DR PROSITE: PS00301; EFACITOR_GTP_1.
KW GTP-binding.
SQ SEQUENCE 639 AA; 72537 MW; 54096C17047F9865 CRC64;

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Query Match 48.3%; Score 43; DB 2; Length 639;
Best local Similarity 50.0%; Pred. No. 67;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 LGTPQPLQVMEP 14
DB 339 IENPHPLQTTVER 352

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Search completed: July 31, 2002, 15:27:00  
Job time: 213 sec